

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:24:57 ; Search time 76.45 Seconds

(without alignments)
196,868 Million cell updates/sec

Title: US-09-351-778A-10

Sequence: 1 MGSRTAPRTDYRMTATGL.....RPPIRPIGLKPCSLUQYD 87

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriaph:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	79.3	101	12	091023 human adeno
2	53	60.9	101	12	091236 human adeno
3	18	20.7	94	12	012392 human adeno
4	7	8.0	83	11	088422 spiroplasma
5	7	8.0	83	11	088422 spiroplasma
6	7	8.0	87	10	094622 oryza sativ
7	7	8.0	160	16	098268 rhizobium 1
8	7	8.0	160	16	098268 rhizobium m
9	7	8.0	197	16	093567 chlamydia p
10	7	8.0	228	2	09RBX8 pseudomonas
11	7	8.0	245	8	09R3V9 nephroselin
12	7	8.0	316	10	09C9Z6 arabidopsis
13	7	8.0	387	16	099X15 staphylococ
14	7	8.0	391	16	097GC3 clostridium
15	7	8.0	392	10	09AX94 oryza sativ
16	7	8.0	404	5	09VIM7 drosophila

17	7	8.0	490	10	09FSS8 oryza sativ
18	7	8.0	536	5	045994 caenorhabditis
19	7	8.0	604	5	09VQ31 drosophila
20	7	8.0	635	5	09VJ77 drosophila
21	7	8.0	649	5	09NKD0 drosophila
22	7	8.0	965	2	032494 bacteroides
23	7	8.0	1175	16	091356 pseudomonas
24	7	8.0	2689	5	095Y78 leishmania
25	6	6.9	26	4	09BUB3 homo sapien
26	6	6.9	53	13	09YH36 oryza sativ
27	6	6.9	64	2	09F347 streptomyces
28	6	6.9	69	13	09DEC6 gallus gall
29	6	6.9	73	15	087603 chimpanzee
30	6	6.9	76	4	09FEN4 homo sapien
31	6	6.9	77	12	064868 avian adeno
32	6	6.9	82	16	09PCC9 xyloella fas
33	6	6.9	83	16	09PE04 xyloella fas
34	6	6.9	89	10	094J51 oryza sativ
35	6	6.9	89	16	09AA87 caulobacter
36	6	6.9	91	4	09H4V4 homo sapien
37	6	6.9	94	16	09PCH2 xyloella fas
38	6	6.9	94	16	09PCA5 xyloella fas
39	6	6.9	95	11	09OZG8 ratius norv
40	6	6.9	97	3	0977L9 schistosom
41	6	6.9	110	17	097A58 thermoplasma
42	6	6.9	113	16	09K1B1 neisseria m
43	6	6.9	113	16	09JX91 neisseria m
44	6	6.9	115	2	09KXU2 streptomyces
45	6	6.9	115	3	09P8V1 ashyba goss

ALIGNMENTS

RESULT 1
ID 091023 PRELIMINARY; PRT; 101 AA.
AC 091023;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 11.6K PROTEIN.
OS Human adenovirus type 2.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=105;
RA Borchering F., Ping-Akerblom P.;
RT "Adenoviruses of subgenus C with different organ tropism."
DR EMBL, AJ293915; CAC67721.1; -
SQ SEQUENCE 101 AA; 11662 MW; 914F50AC2F8B284F CRC64;

Query Match 79.3%; Score 69; DB 12; Length 101;
Best Local Similarity 100.0%; Pred. No. 2e-66;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 APTDYRMTATGLTSLNLPQYHAFVNDMSLDMMFSTALMFVCLIMWLICCKRRR 66
DB 7 APTDYRMTATGLTSLNLPQYHAFVNDMSLDMMFSTALMFVCLIMWLICCKRRR 66
QY 67 ARPPIRPI 75
DB 67 ARPPIRPI 75
RESULT 2
ID 091236 PRELIMINARY; PRT; 101 AA.
AC 091236;
DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE 11.6K PROTEIN.
 OS Human adenovirus type 2.
 OS Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OS NCBI_TaxID=10515;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PRET.
 RA Borchering F., Pring-Akerlorn P.;
 "Adenoviruses of subgenus C with different organ tropism";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ293913; CAC67704.1; -
 SO SEQUENCE 101 AA; 11704 MW; E13857DC5891E85B CRC64;

Query Match 60.9%; Score 53; DB 12; Length 101;
 Best Local Similarity 100.0%; Pred. No. 3.3e-49;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 ALNLPQVHAFVNDMSLDMWFSIALMFVCLIIIMLICCKRRARPPIYRPI 75
 DB 23 ALNLPQVHAFVNDMSLDMWFSIALMFVCLIIIMLICCKRRARPPIYRPI 75

RESULT 3
 ID 012392 PRELIMINARY; PRT; 94 AA.
 AC 012392;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-JAN-1998 (Tremblrel. 05, Last annotation update)
 DE 11.6K PROTEIN.
 GN AD1/E3-11.6K.
 OS Human adenovirus type 1.
 OS Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OS NCBI_TaxID=10533;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HANNOVER / ADRIAN;
 RC Reichmann H., Scharschmidt E., Gelsler B., Hausmann J., Ortmann D.,
 RA Bauer U., Flunker G., Seidel W.;
 RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y11037; CAA72127.1; -
 DR EMBL: Y11032; CAA71916.1; -
 SO SEQUENCE 94 AA; 10674 MW; D148B5AFE771862 CRC64;

Query Match 20.7%; Score 18; DB 12; Length 94;
 Best Local Similarity 100.0%; Pred. No. 1.4e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 MWFESIALMFVCLIIIMWL 58
 DB 35 MWFESIALMFVCLIIIMWL 52

RESULT 4
 ID 088422 PRELIMINARY; PRT; 83 AA.
 AC 088422;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE SPV1-C74, COMPLETE GENOME.
 OS Spiroplasma virus.
 OS Viruses; unclassified viruses.
 OS NCBI_TaxID=12338;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPV1-C74;
 RA Heber C.M., Aulio P., Bove J., Renaudin J.;
 RA "Spiroplasma citri virus SPV1. Characterization of viral sequences

RT present in the spiroplasma host chromosome";
 RL Curr. Microbiol. 32:1-7(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPV1-C74;
 RA Renaudin J.;
 RA Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U28974; AAA85015.1; -
 SO SEQUENCE 83 AA; 9398 MW; D4969373B02BFFA8 CRC64;

Query Match 8.0%; Score 7; DB 12; Length 83;
 Best Local Similarity 100.0%; Pred. No. 8.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 TGLTSAL 24
 DB 30 TGLTSAL 36

RESULT 5
 ID 09WV20 PRELIMINARY; PRT; 85 AA.
 AC 09WV20;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE PROTEIN TYROSINE PHOSPHATASE EPSILON (FRAGMENT).
 GN PREPESILON.
 OS Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OS NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99115422; PubMed=9914474;
 RA Tanuma N., Nakamura K., Kikuchi K.;
 RA "Distinct promoters control transmembrane and cytosolic protein
 RT tyrosine phosphatase epsilon expression during macrophage
 RT differentiation";
 RL Eur. J. Biochem. 259:46-54(1999).
 DR EMBL: D89173; BAA78711.1; -
 FT NON-TER 85
 FT NON-TER 85
 SO SEQUENCE 85 AA; 9031 MW; CFPD2DABE70A02523 CRC64;

Query Match 8.0%; Score 7; DB 11; Length 85;
 Best Local Similarity 100.0%; Pred. No. 8.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 PCSLLDQ 85
 DB 25 PCSLLDQ 31

RESULT 6
 ID 094H62 PRELIMINARY; PRT; 87 AA.
 AC 094H62;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE HYPOHETICAL 9.9 KDA PROTEIN.
 OS Oryza sativa (Rice).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euryhalidae; Oryzae; Oryza.
 OS NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Bell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,

RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tairin T.,
 RA Riggs F., Hsiao J., Zisman V., Blunt S., Pal G., Vanaken S.E.,
 RA Uterback T.R., Feldblum T.V., Quackenbush J., Salzberg S.L.,
 RA White O., Fraser C.M.;
 RT "Oryza sativa chromosome 3 BAC OSJNB0057P11 genomic sequence."
 RL Submitted (MUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC084767; AAK72273.1; -;
 KW Hypothetical protein.
 SO SEQUENCE 87 AA; 9941 MW; 092E2A6E9D0A42CE CRC64;

Query Match 8.0%; Score 7; DB 10; Length 87;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 LKRRAR 68
 DB 48 LKRRAR 54

RESULT 7
 ID 0982G8 PRELIMINARY; PRT; 160 AA.
 AC 0982G8:
 DT 01-OCT-2001 (TReMBLrel. 18, Created)
 DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
 DE 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
 DE MLR9079 PROTEIN.
 GN MLR9079.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Plasmid pML.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 CX NCBI_Taxid=381;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAF303099;
 RA MEDLINE=21082930; PubMed-11214968;
 RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Matanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti."
 RL DNA Res. 7:331-338(2000).
 DR EMBL: AP003015; BAB54491.1; -;
 KM Plasmid; Complete proteome.
 SQ SEQUENCE 160 AA; 17696 MW; 85A9C5A923D9A50 CRC64;

Query Match 8.0%; Score 7; DB 16; Length 160;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGSTIAP 8
 DB 28 TGSTIAP 34

RESULT 8
 ID 092XL7 PRELIMINARY; PRT; 160 AA.
 AC 092XL7:
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE HYPOTHEICAL PROTEIN SMA2279.
 GN SMA2279.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Plasmid pSymb (megaplasmid 1).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.

OX NCBI_Taxid=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396509; PubMed-11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Barlow-Hudler F., Bowser L., Capela D., Galibert F., Guzy J.,
 RA Gujral M., Hong A., Hulzer L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kaiman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 RT Sinorhizobium meliloti pSymb megaplasmid."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 DR EMBL: AE007307; AAK65885.1; -;
 KW Hypothetical protein; Plasmid; Complete proteome.
 SO SEQUENCE 160 AA; 17966 MW; 98B4EBE18A1B34 CRC64;

Query Match 8.0%; Score 7; DB 16; Length 160;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGSTIAP 8
 DB 28 TGSTIAP 34

RESULT 9
 ID 09JSG7 PRELIMINARY; PRT; 197 AA.
 AC 09JSG7:
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE C1142 HYPOTHEICAL PROTEIN_2.
 GN CPJ0259.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 CX NCBI_Taxid=83558;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RA MEDLINE=20330349; PubMed-10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWL029 from USA."
 RL Nucleic Acids Res. 28:2311-2314(2000).
 DR EMBL: AP002545; BAA98469.1; -;
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR InterPro: IPR000531; TonB_boxC.
 DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
 DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
 SQ SEQUENCE 197 AA; 22016 MW; EAA69A27851F790D CRC64;

Query Match 8.0%; Score 7; DB 16; Length 197;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23
 DB 74 ATGLTSA 80

RESULT 10
 ID 09RBX8 PRELIMINARY; PRT; 228 AA.
 AC 09RBX8:
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE HYPOTHEICAL 24.1 KDA PROTEIN.

OS Pseudomonas indologera.
 OC Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Vogesella.
 NCBI_TaxID=45465;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC19706;
 RA van de Loo F.J., Keese P., Llewellyn D.;
 RT "Structural and regulatory genes controlling indigoidine production in
 Vogesella indologera: involvement of a peptide synthetase homolog.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TETR/ACNR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 CC EMBL: AF088856; AAD54003.1;
 DR InterPro: IPR001647; HTR_Tetr.
 DR Pfam: PF00440; tetr; 1.
 DR PRINTS: PR00455; HTRHTR.
 KW DNA-binding; Hypothetical protein; Transcription regulation.
 SO SEQUENCE 228 AA; 2410 MW; A928DE14F040659B CRC64;

Query Match 8.0%; Score 7; DB 2; Length 228;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 RRRAPP 70
 DB 23 RRRAPP 29

RESULT 11
 09T3Y9 PRELIMINARY; PRT; 245 AA.

AC 09T3Y9;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE HYDROTHERMAL 27.2 KDA PROTEIN.
 OS Nephroselmis olivacea.
 OC Chloroplast.
 CC Eukaryota: Viridiplantae: Chlorophyta: Prasinophyceae;
 CC Chlorodendales: Chlorodendraceae; Nephroselmis.
 NCBI_TaxID=31312;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99398694; PubMed-10468594;
 RA Turmel M., Ollis C., Lemieux C.;
 RT "The complete chloroplast DNA sequence of the green alga Nephroselmis
 olivacea: Insights into the architecture of ancestral chloroplast
 genomes.";
 RT Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Turmel M., Ollis C., Lemieux C.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF137379; AAD54918.1;
 DR EMBL: AF137379; AAD54871.1;
 KW Hypothetical protein; Chloroplast.
 SO SEQUENCE 245 AA; 27217 MW; 74FDF5F5F229FF7 CRC64;

Query Match 8.0%; Score 7; DB 8; Length 245;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 TGLTSAL 24
 DB 204 TGLTSAL 210

RESULT 12
 09C9Z6 PRELIMINARY; PRT; 316 AA.
 AC 09C9Z6;

DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE HYDROTHERMAL 34.7 KDA PROTEIN (AT350860/F17014_7).
 GN F17014.7
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots: Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RX MEDLINE-21016720; PubMed-11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unsel M.,
 RA Farman B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA Delseny M., Boutry M., Grivell L.A., Mache R., Pulgomech P.,
 RA De Simone V., Choisme N., Artiguenave F., Robert C., Brodier P.,
 RA Mincker P., Catolico L., Weissbach J., Saurin W., Queller F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wumbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
 RA Wedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppe S., Simonelli B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T.H., Nordstiek G.,
 RA Reichelt J., Scharte M., Schuen O., Bargues M., Terol J., Climent J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
 RA Cooke R., Landie M., Berger-Liauro C., Purnelle B., Masuy D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 RA Monfort A., Argitrou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haese D., Schoof H., Ruid S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii S., Shea T.P.,
 RA Creasy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
 RA Pal G., Miltner J., Sellers P., Gill J.E., Feldlyan T.V.,
 RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Aamzu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 thaliana.";
 RT Nature 408:820-822(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carlini P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamuya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis ORF clones.";
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carlini P., Dale J.M., Gibson H.A., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamuya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
 RA Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis cDNA clones.";
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC012562; AAC51364.1;
 DR EMBL: AY056087; AAL06873.1;
 DR EMBL: AY045678; AAK74036.1;
 KW Hypothetical protein.
 SO SEQUENCE 316 AA; 34732 MW; 5B54FCCF59A5B5B CRC64;

Query Match 8.0%; Score 7; DB 10; Length 316;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 LLSALNPQ 28
 |||||
 DB 146 SALNPQ 152

RESULT 13

O99X15 PRELIMINARY; PRT: 387 AA.

AC O99X15;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE SA0200 PROTEIN (HYPOTHETICAL PROTEIN SAV0207).
 GN SA0200 OR SAV0207.
 OS Staphylococcus aureus (strain N315), and
 OC Staphylococcus aureus (strain Mu50).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 OX NCBI_TaxID=158879, 158878;

RN [1]
 RM SEQUENCE FROM N.A.
 RP SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50);
 RC MEDLINE=21311952; PubMed=1418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Imai J.-O., Ito T.,
 RA Kanamori M., Matsunari H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mitani-Uchi Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yahasaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 DR EMBL: AP003129; BAB41422.1;
 DR EMBL: AP003358; BAB56369.1;
 DR InterPro: IPR000515; BPD.transp.
 DR Pfam: PF00528; BPD.transp.1.
 KW Complete proteome; Hypothetical protein
 SQ SEQUENCE 387 AA; 43077 MW; 08f9fb4bca6dc8 CRC64;

Query Match 8.0%; Score 7; DB 16; Length 387;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 LLSALNL 26
 |||||
 DB 27 LLSALNL 33

RESULT 14

O97GC3 PRELIMINARY; PRT: 391 AA.

AC O97GC3;
 DT 01-OCT-2001 (TREMblrel. 18, Created)
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE AICAR TRANSFORMYLASE DOMAIN OF PURH-LIKE PROTEIN.
 GN CAC2445.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium
 OX NCBI_TaxID=1488;
 RN [1]
 RM SEQUENCE FROM N.A.
 RP STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RC MEDLINE=21359325; PubMed=11466286;
 RX Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

RA Gibson R., Lee H.M., Dubois J., Qiu D., Hatt J., Wolf Y.I.,
 RA Tatusov R.L., Sabate F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum."
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL: AE007744; AAK80399.1;
 DR InterPro: IPR002695; AICARFT_IMPCHas.
 DR Pfam: PF01808; AICARFT_IMPCHas.1.
 DR ProDom: PD004666; AICARFT_IMPCHas.1.
 KW Complete proteome.
 SQ SEQUENCE 391 AA; 43547 MW; 18642c6ba97e909e CRC64;

Query Match 8.0%; Score 7; DB 16; Length 391;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23
 |||||
 DB 58 ATGLTSA 64

RESULT 15

O9AX94 PRELIMINARY; PRT: 392 AA.

AC O9AX94;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE P0501G01.23 PROTEIN.
 GN P0501G01.23
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriactoidae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RM SEQUENCE FROM N.A.
 RP STRAIN=CV. NIPPONBARE;
 RC Sasaki T., Matsumoto T., Yamamoto K.;
 RA "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone: P0501G01."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP002819; BAB21094.1;
 SQ SEQUENCE 392 AA; 40501 MW; BB4f44827a7EDC34 CRC64;

Query Match 8.0%; Score 7; DB 10; Length 392;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 RRRARPP 70
 |||||
 DB 133 RRRARPP 139

Search completed: June 21, 2002, 08:24:57
 Job time: 282 sec
